

DNA sequence encoding mRNA	siRNA Duplex Structure
STAT6(1): AAGCAGGAAGAACTCAAGTTT→	5'-GCAGGAAGAACUCAAGUUUtt-3' 3'-ttCGUCCUUCUUGAGUUCAAA-5'
[SEQ ID No.15]	[SEQ ID No.1]
STAT6(2): AAACAGTACGTTACTAGCCTT→	5'-ACAGUACGUUACUAGCCUUtt-3' 3'-ttUGUCAUGCAAUGAUCGGAA-5'
[SEQ ID No.16]	[SEQ ID No.2]
STAT6(3): AAGAATCAGTCAACGTGTTGT→	5'-GAAUCAGUCAACGUGUUGUtt-3' 3'-ttCUUAGUCAGUUGCACAACA-5'
[SEQ ID No.17]	[SEQ ID No.3]
STAT6(4): AAAGCACTGGAGAAATCATGA→	5'-AGCACUGGAGAAAUCAUCAtt-3' 3'-ttUCGUGACCUCUUUAGUAGU-5'
[SEQ ID No.18]	[SEQ ID No.4]

Figure 1

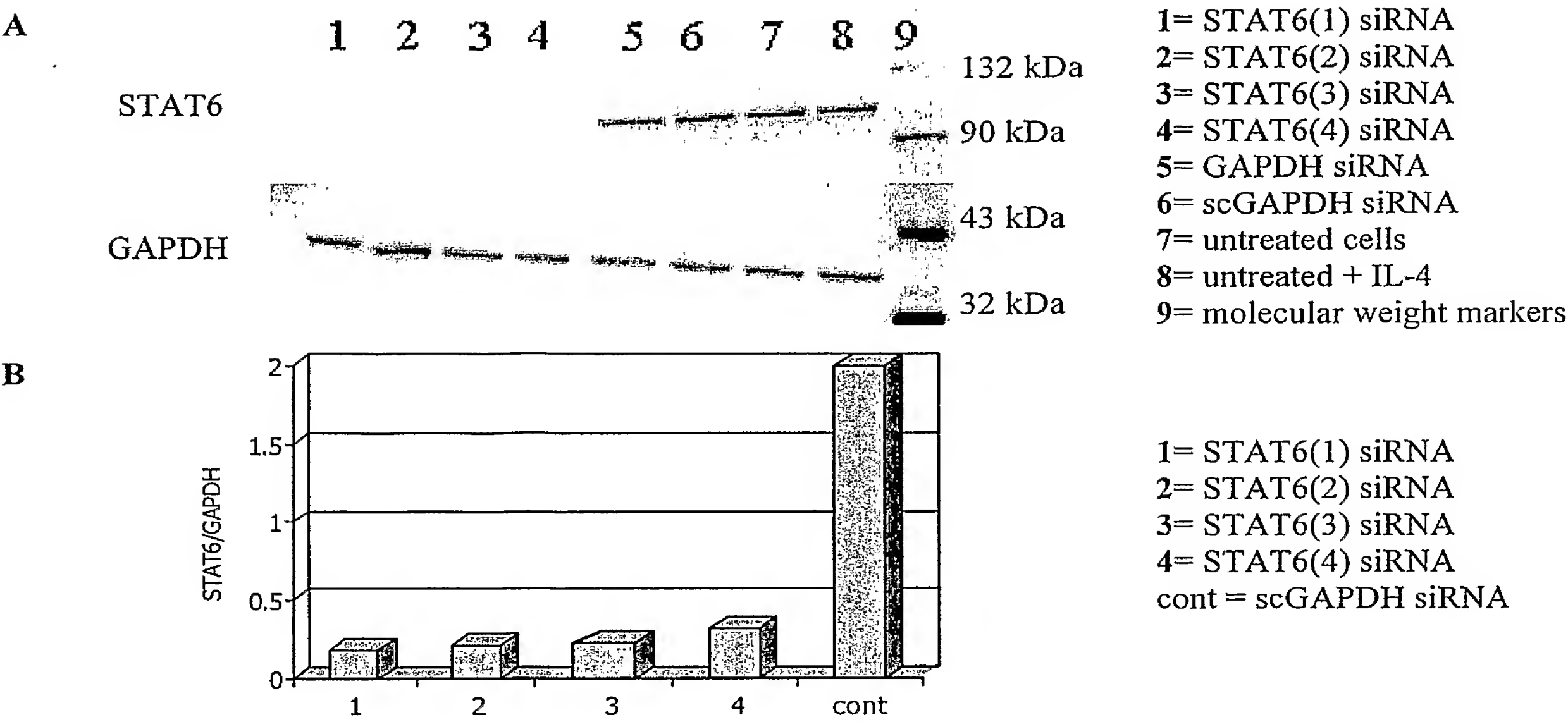


Figure 2

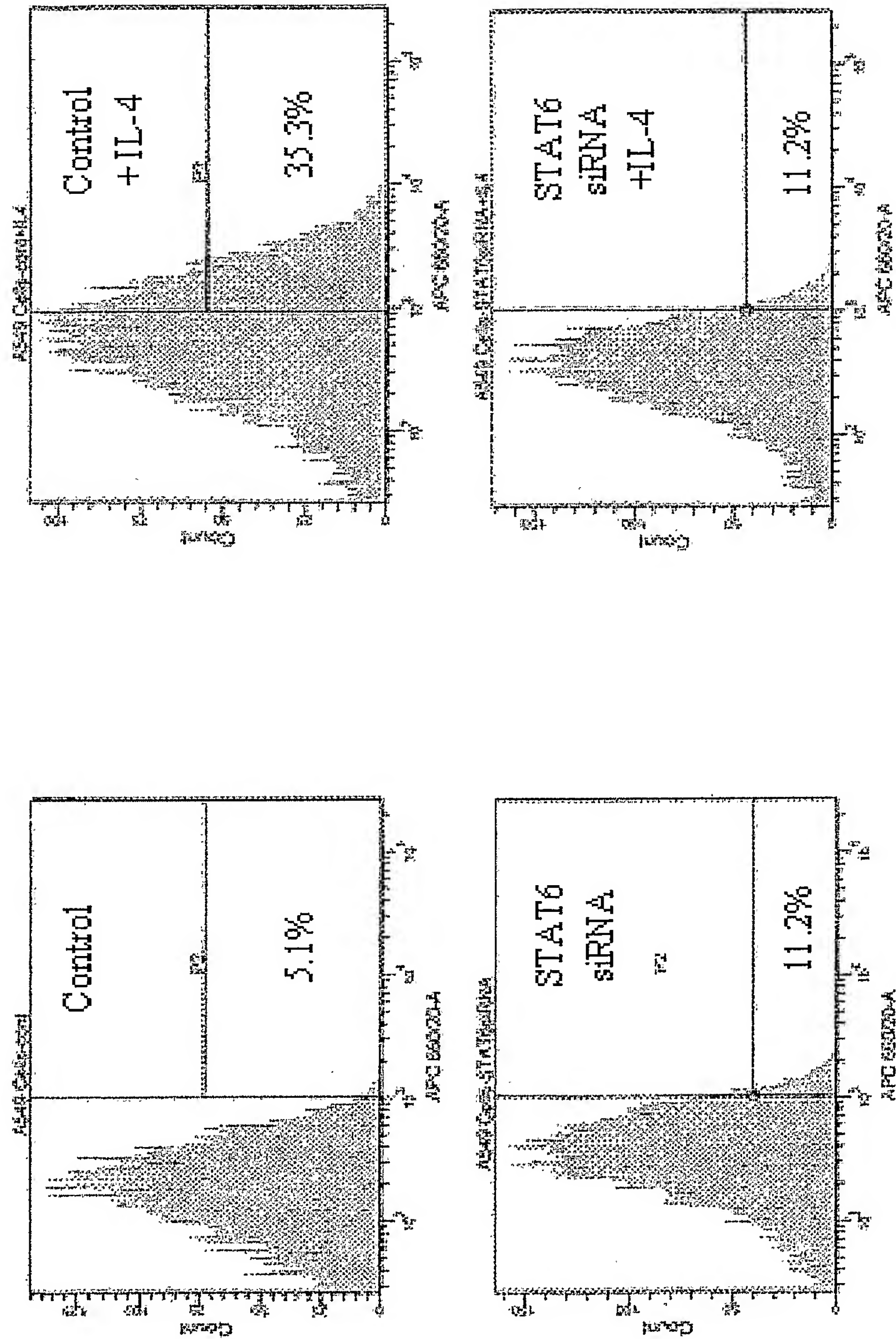


Figure 3

NM 003153 [gi:23397677]

LOCUS NM_003153 3993 bp mRNA linear PRI 27-OCT-2004
 DEFINITION Homo sapiens signal transducer and activator of transcription 6,
 interleukin-4 induced (STAT6), mRNA.
 ACCESSION NM_003153
 VERSION NM_003153.3 GI:23397677
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
 reference sequence was derived from BC005823.2 and BQ028928.1.
 On Oct 1, 2002 this sequence version replaced gi:21536302.

Summary: The protein encoded by this gene is a member of the STAT family of transcription factors. In response to cytokines and growth factors, STAT family members are phosphorylated by the receptor associated kinases, and then form homo- or heterodimers that translocate to the cell nucleus where they act as transcription activators. This protein plays a central role in exerting IL4 mediated biological responses. It is found to induce the expression of BCL2L1/BCL-X(L), which is responsible for the anti-apoptotic activity of IL4. Knockout studies in mice suggested the roles of this gene in differentiation of T helper 2 (Th2) cells, expression of cell surface markers, and class switch of immunoglobulins.

FEATURES Location/Qualifiers
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 go_function: signal transducer activity [goid 0004871]
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 go_function: transcription factor activity [goid 0003700]

Figure 4

[evidence TAS] [pmid 10747856];
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Figure 4 (continued)

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ORIGIN

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Figure 4 (continued)

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Figure 4 (continued)

NM 009284 [gi:6678154]

LOCUS NM_009284 3213 bp mRNA linear ROD 28-OCT-2004
 DEFINITION Mus musculus signal transducer and activator of transcription 6
 (Stat6), mRNA.
 ACCESSION NM_009284
 VERSION NM_009284.1 GI:6678154
 KEYWORDS .
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from L47650.1.
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Figure 5

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ORIGIN

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Figure 5 (continued)

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Figure 5 (continued)

XM 343223 [gi:34865760]

LOCUS XM_343223 2442 bp mRNA linear ROD 24-OCT-2003

DEFINITION Rattus norvegicus similar to signal transducer and activator of transcription 6 (LOC362896), mRNA.

ACCESSION XM_343223

VERSION XM_343223.1 GI:34865760

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence (NW_047777) using gene prediction method: GNOMON, supported by EST evidence.

Also see:

Documentation of NCBI's Annotation Process

FEATURES Location/Qualifiers

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Figure 6

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 GRGFTFWQWFDGVLDLTKRCLRSYWSDRLIIGFISKQYVTSLLLNEPDGTFLLRFS
 EIGGITIAHVIRGQDGSSQIENIQPFSAKDLSIRSLGDRIRDLAQLKNLYPKKPKDEA
 FRSHYKPEQMGKDGRGYVSTTIKMTVERDQPLPTPEPQMPAMVAPYDLGMAPDASMQL
 SSDMVPHLQMPPTMSQISMPFDQPHPQGGLQCQSQEHA VSSPELLCSDVTMAEDSCL
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GISMSHLDLRTNPSW" [SEQ ID No.13]

misc feature 4..348

/gene="LOC362896"

/note="STAT_prot; Region: STAT protein, protein interaction domain. STAT proteins (Signal Transducers and Activators of Transcription) are a family of transcription factors that are specifically activated to regulate gene transcription when cells encounter cytokines and growth factors. STAT proteins also include an SH2 domain pfam00017"

/db_xref="CDD:pfam02865"

misc feature 370..813

/gene="LOC362896"

/note="STAT; Region: STAT protein, all-alpha domain. STAT proteins (Signal Transducers and Activators of Transcription) are a family of transcription factors that are specifically activated to regulate gene transcription when cells encounter cytokines and growth factors. STAT proteins also include an SH2 domain pfam00017"

/db_xref="CDD:pfam01017"

misc feature 817..1581

/gene="LOC362896"

/note="STAT_bind; Region: STAT protein, DNA binding domain. STAT proteins (Signal Transducers and Activators of Transcription) are a family of transcription factors that are specifically activated to regulate gene transcription when cells encounter cytokines and growth factors. This family represents the DNA binding domain of STAT, which has an ig-like fold. STAT proteins also

Figure 6 (continued)

include an SH2 domain pfam00017"
 /db_xref="CDD:pfam02864"
 misc feature 1612..1848
 /gene="LOC362896"
 /note="SH2; Region: SH2 domain"
 /db_xref="CDD:pfam00017"
 misc feature 1618..1860
 /gene="LOC362896"
 /note="SH2; Region: Src homology 2 domains"
 /db_xref="CDD:smart00252"

ORIGIN

1 atgtctctgt ggagtctagt ttccaagatg tccccagaaa aactgcaacg gctctatgtt
 61 gactttccac aacacctgcg gcatcttctg gccgaatggc tggagaatca gccctgggag
 121 ttctgggtg gttcagatgc ttctgttac aacatggcta gtgccctact ttctgccact
 181 gtccagcgtc ttcaggcctc tgcaggagag caggggaaag gaagcagcct cttgcagcac
 241 atcagcacct tggagagcat ctatcagagg gacccccctga agctgggtggc caccatcaga
 301 caaatacttc aagggggagaa aaaagctgtt atagaagagt tccaccacct gccagggccc
 361 ttccatcgaa agcaggaaga actcaagttt actacagccc tgggcaggct tcagcaccga
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 2161 gtgtccagcc ctgaacctt gctgtgttca gatgtacta tggcggaaga cagctgccta
 2221 actcagcctg tgcaagggtt cccccagggc acctgggtca gcgaaggcat gtacctccc
 2281 ctgatgcctc ccactgaaca ggacctacc aagcttctcc tagagggcca aggggaagg

Figure 6 (continued)

2341 ggaggatcca tagggactca gcccctcctg caaccatctt cttatgggca atcggggatc
2401 tcaatgtccc acctggacct aaggaccaac cccagttggt ga [SEQ ID No.14]

Figure 6 (continued)

SUBSTITUTE SHEET (RULE 26)

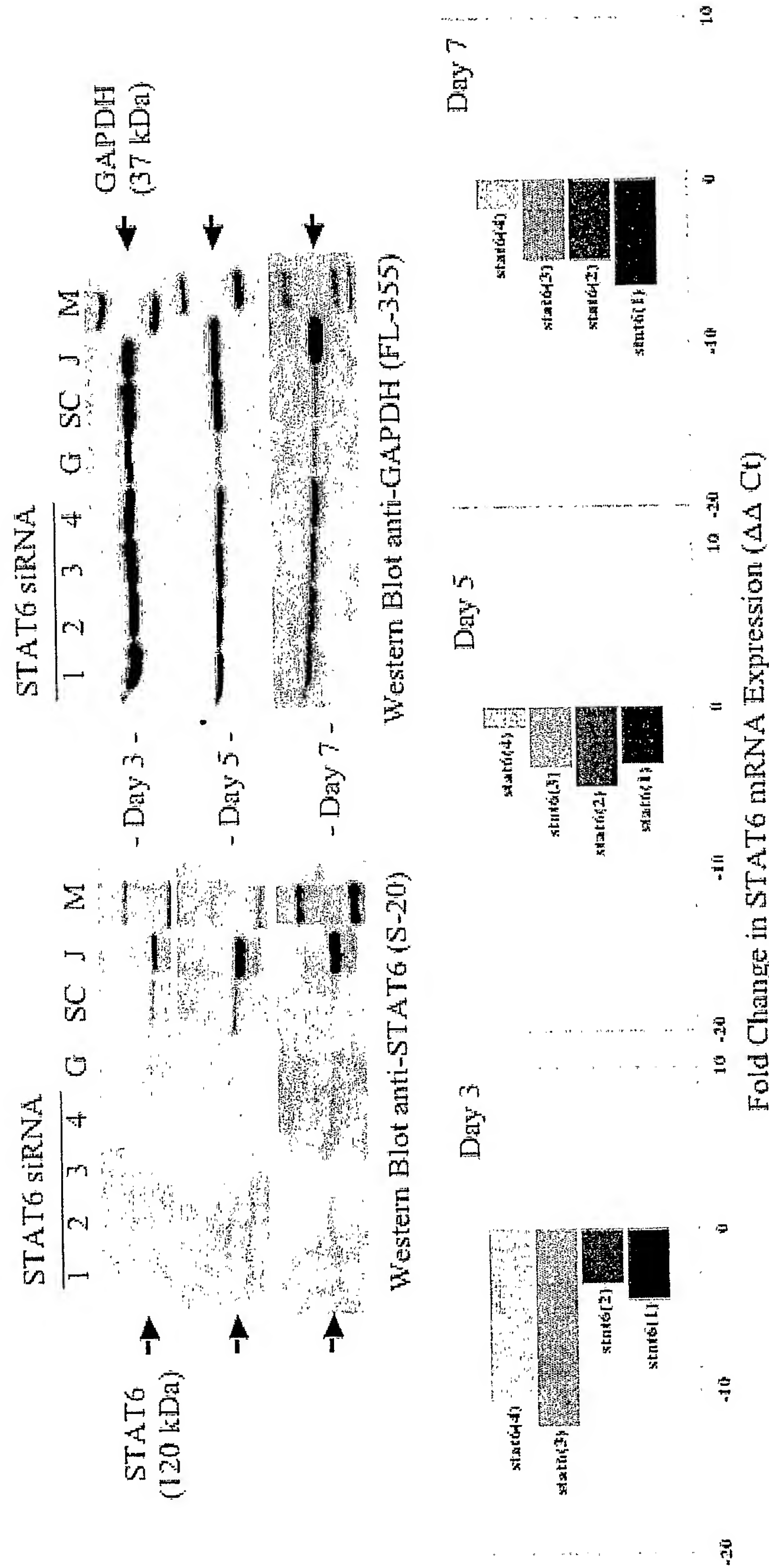


Figure 7

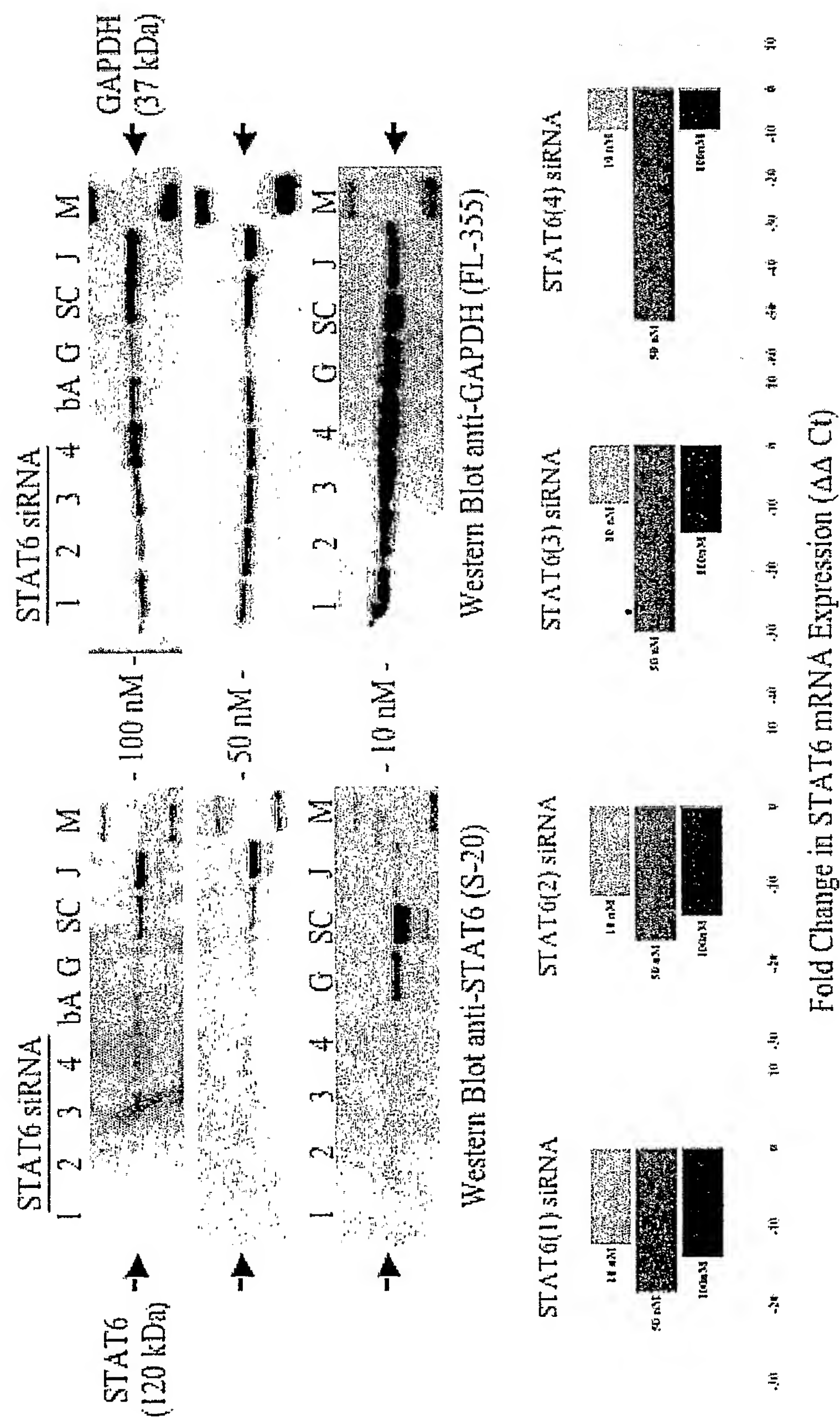


Figure 8

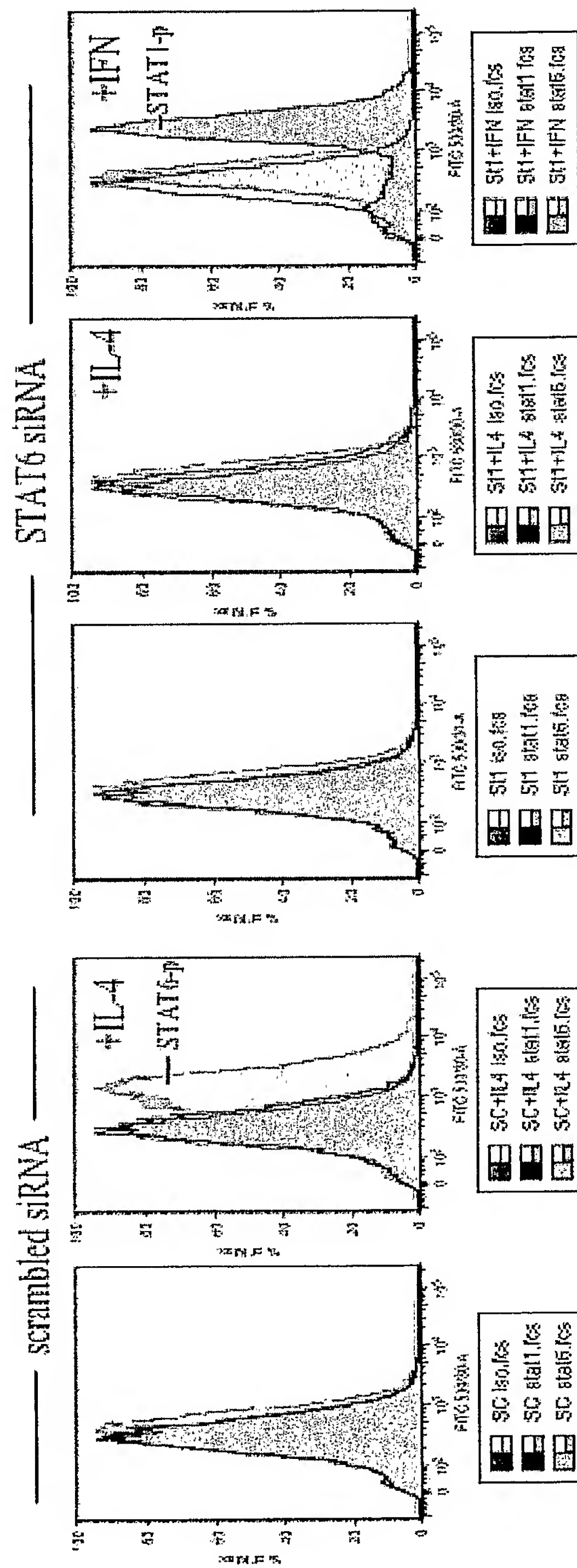


Figure 9

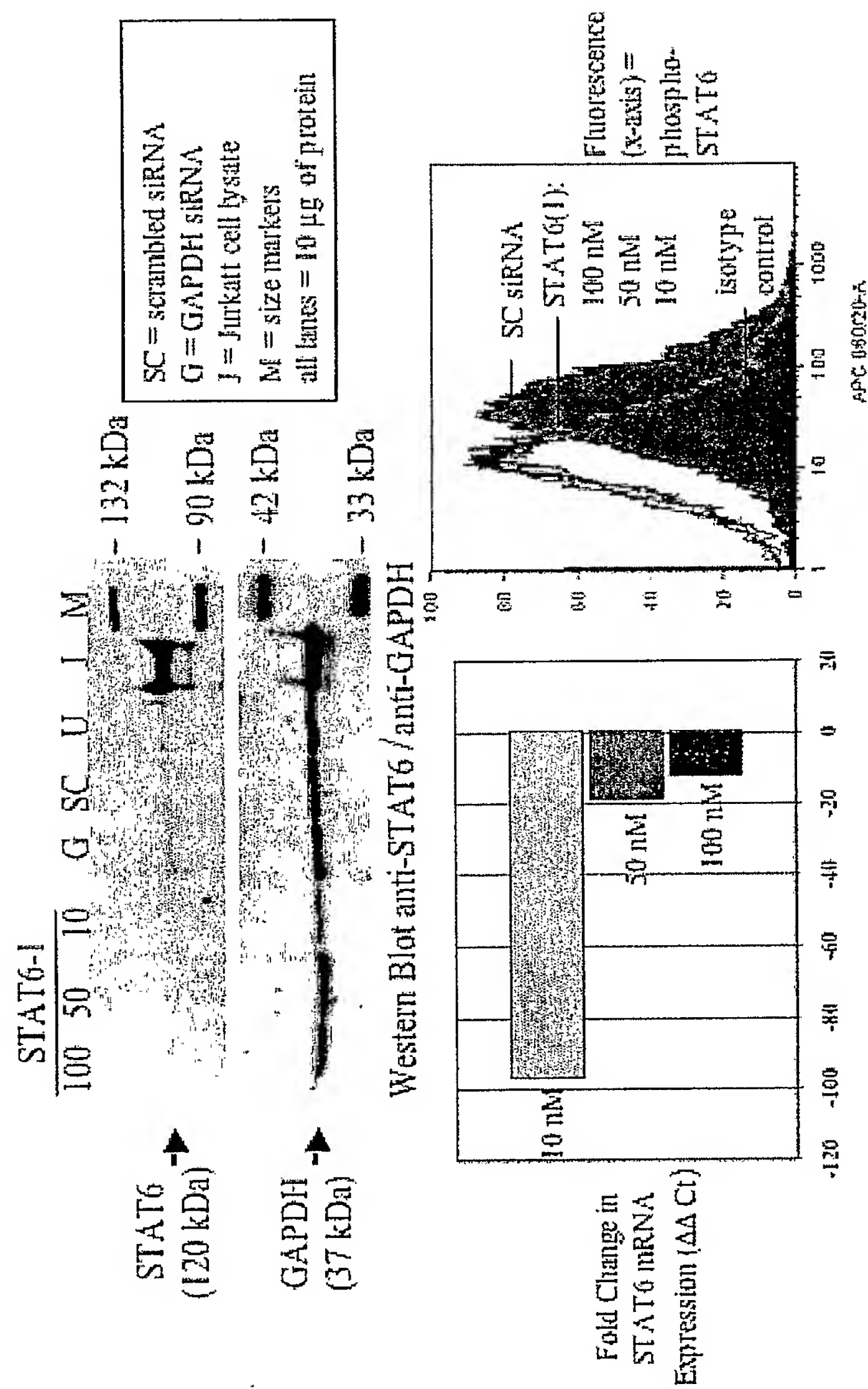


Figure 10

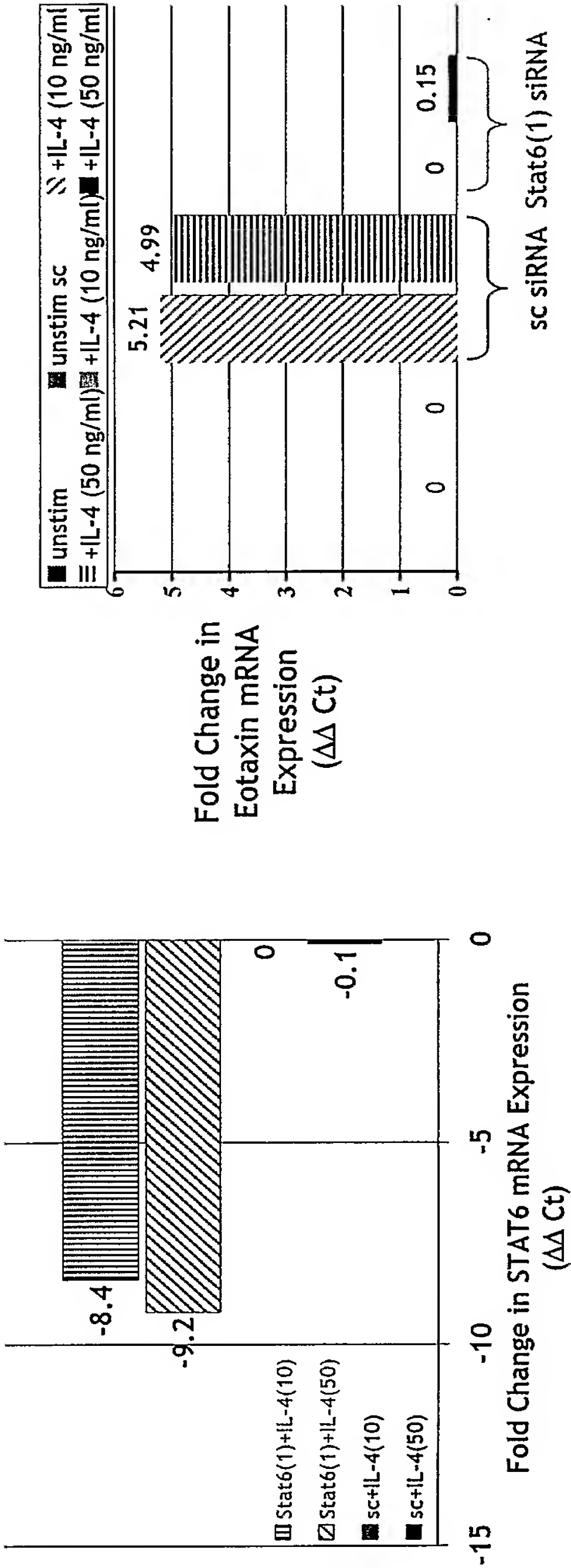


Figure 11